Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims

1. (currently amended) A method for determining the extent of degradation ~~quality~~, expressed in terms of a quality value, of ~~an~~ biomolecule sample, ~~based on measured data of the biomolecule sample, the~~ method comprising:[[:]]

separating the biomolecule sample by one or more molecular characteristics, using a device, to generate measured data,

extracting a number of prescribed features from the measured data using data analysis, and

determining the quality value, which indicates the extent of degradation of the biomolecule sample, from the extracted features using a quality algorithm,

wherein the quality algorithm has been derived from:

collecting a statistically significant number of trial measured data covering a prescribed set of biomolecule samples,

assigning a quality label, which indicates the extent that the trial measured data exhibits signs of degradation, to every trial measured data

extracting features from the trial measured data using data analysis,

determining functional interrelations among the quality labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation, and

specifying the functional interrelation that has the highest rating factor as the quality algorithm.

2. (currently amended) The method of claim 1, further comprising ~~at least one of the features~~:

specifying one or more anomalous cases ~~are specified~~ from among a prescribed number of potentially anomalous cases,

extracting a number of prescribed features ~~are extracted~~ from the measured data of the biomolecule sample using data analysis for every anomalous case,

analyzing the measured data ~~is analyzed~~ using an associated anomalous-case algorithm in order to validate every anomalous case identified, and

determining the magnitude of the anomaly involved ~~is determined~~ from a combination of the anomalous cases present in order to determine the degree to which the biomolecule sample is anomalous.

3. (previously presented) The method of claim 1, wherein the functional interrelations among the quality labels and the various combinations of extracted features are determined using an adaptive approach.

4. (currently amended) The method of claim 2, wherein the following is carried out in order to determine the anomalous-case algorithm for a prescribed anomalous case:

collecting a statistically significant number of trial measured data covering a prescribed set of biomolecule samples,

assigning an anomalous-case label, which indicates the magnitude of anomaly, to the prescribed anomalous case of every trial measured data,

extracting features from the trial measured data using data analysis,

determining functional interrelations among the anomalous-case labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation, and

specifying the function interrelation that has the highest rating factor as the anomalous-case algorithm.

5. (previously presented) The method of claim 4, wherein the functional interrelations among the anomalous-case labels and the various combinations of extracted features are determined using an adaptive approach.

6. (original) The method of claim 1, wherein discrete classes are established for the accessible range of measured data quality and every class is assigned a quality label.

7. (previously presented) The method of claim 6, wherein seven classes are established for the quality label.

8. (original) The method of claim 4, wherein 0 and 1 are prescribed as allowed values of the anomalous-case label.

9. (original) The method of claim 1, wherein the measured data are subdivided into segments in order to extract features therefrom.

10. (currently amended) The method of claim 9, wherein the biomolecule sample is an RNA sample, and the following eight regions of the measured data of the RNA sample are

established as the segments: a preregion, a marker region, a 5S-region, a fast region, an 18S-region, an interregion, a 28S-region, and a postregion.

11. (currently amended) The method of claim 1, wherein ~~the~~ positions, heights, and widths of peaks occurring in the measured data are determined and their areas computed by integration under the data analysis performed on the measured data.

12. (currently amended) The method of claim 9, wherein the measured data can be represented as a data curve or a smoothed data curve and wherein one or more of the following ~~local~~ prescribed features of segments of the data curve, or the smoothed data curve, of the measured data are determined in the data analysis of the measured data:

the maximum and minimum value occurring within the segment,

the slope and y-intercept of the interpolating straight line fitted to the points on the curve falling within the bounds of the segment,

the y-values of this interpolating straight line at the start and end points of the segment,

the area under the curve,

the area under the interpolating straight line, the ratios of the latter areas to the area under the entire data curve,

the deviation of the interpolating straight line from the data curve, ~~and/~~or

the deviations of the original and smoothed data curve from one another.

13. (previously presented) The method of claim 12, wherein Savitzky-Golay filters and/or the rolling-ball algorithm are employed for smoothing the data curve.

14. (original) The method of claim ~~9~~ 10, wherein the biomolecule sample is an RNA sample, and one or more of the following ~~global~~ prescribed features are determined in the data analysis of the measured data:

the ratio of the areas of the 18S ~~fragment~~region and 28S ~~fragment~~region to the total area enclosed within the ~~utilized section~~ eight segments,

the ratio of the area of the 18S ~~fragment~~region to the area of the 28S ~~fragment~~region, ~~and~~/or

the signal/noise ratio.

15. (currently amended) The method of claim ~~1~~ 4, wherein the extracted features are consecutively arranged in a list such that the information on the quality label and/or the anomalous-case label will be progressively maximized as each additional feature is added, where each addition of a feature to the list defines a new combination of features.

16. (currently amended) The method of ~~preceding~~ claim 15, wherein the arrangement of extracted features in the list is based on mutual information.

17. (original) The method of claim 3, wherein a neural network is employed as the adaptive approach.

18. (previously presented) The method of claim 17, wherein a Bayesian method is applied for adjusting parameters for the neural network.

19. (original) The method of claim 17, wherein functional interrelations of varying complexity are determined, where the necessary complexity of the functional

interrelations sought is obtained by iterative additions of hidden neurons to the neuronal network.

20. (currently amended) The method of claim 18, wherein the a-posteriori probability of the neuronal network computed using a Bayesian method is employed as the rating factor.

21. (currently amended) The method of claim 1, wherein the biomolecule sample comprises at least one sample selected from the ~~of a~~ group consisting of ~~comprising:~~ an RNA sample, a DNA sample, a protein sample, a peptide sample, a sugar sample, a lipid sample, and a modified form of one or more of the aforementioned biomolecule samples.

22. (currently amended) The method of claim 1, wherein the biomolecule sample comprises ~~representatives of one or more of the known~~ at least one biomolecule type~~s~~ selected from the group consisting of~~, such as~~ RNA molecules, DNA molecules, protein molecules, peptides, sugars, ~~or~~ lipids, and ~~including~~ modified forms of the former biomolecules.

23. (canceled)

24. (original) The method of claim 1, wherein the measured data is an electropherogram.

25. (currently amended) A ~~software program or product, preferably stored on a~~ non-transitory computer-readable data carrier, for executing or controlling a method for determining the extent of degradation ~~quality~~, expressed in terms of a quality value, of ~~an~~ biomolecule sample based on measured data of the biomolecule sample, the method comprising:

extracting a number of prescribed features from the measured data using data analysis, and

determining the quality value, which indicates the extent of degradation of the biomolecule sample, from the extracted features using a quality algorithm,

wherein the quality algorithm has been derived from:

collecting a statistically significant number of trial measured data covering a prescribed set of biomolecule samples,

assigning a quality label, which indicates the extent that the trial measured data exhibits signs of degradation, to every trial measured data,

extracting features from the trial measured data using data analysis,

determining functional interrelations among the quality labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation and

specifying the functional interrelation that has the highest rating factor as the quality algorithm, when run on a data processing system such as a computer.

26. (currently amended) An apparatus for determining the extent of degradation ~~quality~~, expressed in terms of a quality value, of a biomolecule sample, based on measured data of the biomolecule sample, the apparatus comprising: a processing unit adapted for extracting a number of prescribed features from the measured data using data analysis, and for determining the quality value, which indicates the extent of degradation of the biomolecule sample, from the extracted features using a quality algorithm, wherein the quality algorithm has been derived from:

collecting a statistically significant number of trial measured data covering a prescribed set of biomolecule samples,

assigning a quality label, which indicates the extent that the trial measured data exhibits signs of degradation, to every trial measured data,

extracting features from the trial measured data using data analysis,

determining functional interrelations among the quality labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation and

specifying the functional interrelation that has the highest rating factor as the quality algorithm, when run on a data processing system such as a computer.

27. (new) A method for determining the extent of degradation, expressed in terms of a quality value, of an RNA sample, the method comprising:

separating the RNA sample by mobility, using an electrophoresis device, to generate an electropherogram,

extracting a number of prescribed features from the electropherogram using data analysis, and

determining the quality value, which indicates the extent of degradation of the RNA sample, from the extracted features using a quality algorithm,

wherein the quality algorithm has been derived from:

collecting a statistically significant number of trial RNA electropherograms covering a prescribed set of RNA samples,

assigning a quality label, which indicates the extent that the electropherograms exhibit signs of degradation, to every electropherogram,

extracting features from the electropherograms using data analysis,

determining functional interrelations among the quality labels and one or more combinations of the extracted features,

assigning a rating factor to every functional interrelation, and

specifying the functional interrelation that has the highest rating factor as the quality algorithm.

28. (new) A method for determining the extent of degradation, expressed in terms of a quality value, of an RNA sample, the method comprising:

separating the RNA sample by mobility, using an electrophoresis device, to generate an electropherogram,

extracting a number of prescribed features from the electropherogram using data analysis, and

determining the quality value, which indicates the extent of degradation of the RNA sample, from the extracted features using a quality algorithm,

wherein the quality algorithm has been derived by mathematical modeling from a statistically significant number of trial RNA electropherograms covering a prescribed set of RNA samples.

29. (new) A method for determining the extent of degradation, expressed in terms of a quality value, of an RNA sample, the method comprising:

separating the RNA sample by mobility, using an electrophoresis device, to generate an electropherogram,

subdividing the eletropherogram into segments comprising an 18S-region, a 28S-region, and at least one region selected from the group consisting of a preregion, a marker region, a 5S-region, a fast region, an interregion, and a postregion,

extracting a number of prescribed features from the electropherogram using data analysis, wherein at least some of the prescribed features are extracted from the segments of the electropherogram, and

determining the quality value, which indicates the extent of degradation of the RNA sample, from the extracted features using a quality algorithm.

30. (new) A method for determining the extent of degradation, expressed in terms of a quality value, of a biomolecule sample, the method comprising:

separating the biomolecule sample by one or more molecular characteristics, using a device, to generate measured data,

extracting a number of prescribed features from the measured data using data analysis, and

determining the quality value, which indicates the extent of degradation of the biomolecule sample, from the extracted features using a quality algorithm.

31. (new) The method of claim 30, wherein the biomolecule sample is an RNA sample and the measured data is an electropherogram.

32. (new) The method of claim 31, wherein the electropherogram is subdivided into segments to extract features therefrom.

33. (new) The method of claim 32, wherein the segments comprise a fast region, an 18S-region, and a 28S-region.

34. (new) The method of claim 33, wherein the electropherogram can be represented as a data curve or a smoothed data curve and wherein one or more of the following prescribed features from the segments of the data curve, or the smoothed data curve, of the electropherogram are determined in the data analysis of the electropherogram:

the maximum and minimum value occurring within the segment,

the slope and y-intercept of the interpolating straight line fitted to the points on the curve falling within the bounds of the segment,

the y-values of this interpolating straight line at the start and end points of the segment,

the area under the curve,

the area under the interpolating straight line, the ratios of the latter areas to the area under the entire data curve,

the deviation of the interpolating straight line from the data curve, or

the deviations of the original and smoothed data curve from one another.